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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:36:52 ; Search time 11 Seconds
(without alignments)
41.789 Million cell updates/sec

Title: US-10-646-770-2

Perfect score: 96

Sequence: 1 MCTKSLLLAALMSVLLHL.....PKQTWVKYIVRLLSKVKQNM 96

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 26661 seqs, 4788334 residues

Word size : 6

Total number of hits satisfying chosen parameters: 33

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	7.3	265	6	US-10-793-626-2500
2	7	7.3	345	6	US-10-467-657-7598
3	7	7.3	419	6	US-10-467-657-8064
4	7	7.3	488	6	US-10-821-234-1000
5	7	7.3	697	7	US-11-082-389-362
6	6	6.2	87	6	US-10-467-657-8698
7	6	6.2	140	6	US-10-467-657-7270
8	6	6.2	177	6	US-10-980-388-94
9	6	6.2	182	7	US-11-074-176-246
10	6	6.2	229	6	US-10-131-826A-410
11	6	6.2	229	6	US-10-467-657-5756
12	6	6.2	243	6	US-10-467-657-3362
13	6	6.2	276	6	US-10-467-657-6
14	6	6.2	276	6	US-10-467-657-4158
15	6	6.2	281	6	US-10-131-826A-54
16	6	6.2	323	6	US-10-821-234-981
17	6	6.2	337	6	US-10-980-388-115
18	6	6.2	348	6	US-10-467-657-8200
19	6	6.2	356	6	US-10-467-657-4740
20	6	6.2	358	6	US-10-793-626-2136
21	6	6.2	358	6	US-10-980-388-96
22	6	6.2	365	6	US-10-793-626-470
23	6	6.2	365	7	US-11-108-528-56
24	6	6.2	365	7	US-11-108-528-58
25	6	6.2	389	6	US-10-980-388-116

Sequence 1520, Ap
Sequence 921, Appli
Sequence 1, Appli
Sequence 20, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 4, Appli
Sequence 67, Appl

ALIGNMENTS

RESULT 1

US-10-793-626-2500
; Sequence 2500, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2500
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2500

Query Match 7.3%; Score 7; DB 6; Length 265;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 ROLANEG 57
|||||||
Db 205 ROLANEG 211

RESULT 2

US-10-467-657-7598
; Sequence 7598, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7598
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7598

Query Match 7.3%; Score 7; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 7 LLLAALM 13
Db 159 LLLAALM 165

RESULT 3
US-10-467-657-8064
; Sequence 8064, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8064
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8064

Query Match 7.3%; Score 7; DB 6; Length 419;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SLLAAL 12
Db 78 SLLAAL 84

RESULT 4
US-10-821-234-1000
; Sequence 1000, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1000
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1000

Query Match 7.3%; Score 7; DB 6; Length 488;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SLLAAL 12
Db 31 SLLAAL 37

RESULT 5
US-11-082-389-362
; Sequence 362, Application US/11082389

; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 362
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-362

Query Match 7.3%; Score 7; DB 7; Length 697;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LAALMSV 15
Db 322 LAALMSV 328

RESULT 6
US-10-467-657-8698
; Sequence 8698, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8698
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8698
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Query Match 6.2%; Score 6; DB 6; Length 87;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SLLAA 11
Db 76 SLLAA 81
|||||

RESULT 7
US-10-467-657-7270
; Sequence 7270, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7270
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7270

Query Match 6.2%; Score 6; DB 6; Length 140;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLLAAL 12
Db 7 LLLAAL 12
|||||

RESULT 8
US-10-980-388-94
; Sequence 94, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325 US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880

PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/217,369
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/217,370
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/218,492
PRIOR FILING DATE: 2000-07-20
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.0
SEQ ID NO 94
LENGTH: 177
TYPE: PRT
ORGANISM: Homo sapiens
US-10-980-388-94

Query Match 6.2%; Score 6; DB 6; Length 177;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLLAAL 12
Db 119 LLLAAL 124
|||||

RESULT 9
US-11-074-176-246
; Sequence 246, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-246

Query Match 6.2%; Score 6; DB 7; Length 182;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 AASNF 31
Db 146 AASNF 151
|||||

RESULT 10
US-10-131-826A-410
; Sequence 410, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

APPLICANT: Gurney,Austin L.
APPLICANT: Sherwood,Steven
APPLICANT: Smith,Victoria
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131.826A
PRIORITY FILING DATE: 2002-04-24
PRIORITY APPLICATION NUMBER: 60/049911
PRIORITY FILING DATE: 1997-06-18
PRIORITY APPLICATION NUMBER: 60/056974
PRIORITY FILING DATE: 1997-08-26
PRIORITY APPLICATION NUMBER: 60/059113
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059115
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059117
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059122
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059184
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059263
PRIORITY FILING DATE: 1997-09-18
PRIORITY APPLICATION NUMBER: 60/059352
PRIORITY FILING DATE: 1997-09-19
PRIORITY APPLICATION NUMBER: 60/059588
PRIORITY FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 410
LENGTH: 229
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-826A-410

Query Match 6.2%; Score 6; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLLAAL 12
Db 12 LLLAAL 17

RESULT 11
US-10-467-657-5756
Sequence 5756, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 5756
LENGTH: 229
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5756

Query Match 6.2%; Score 6; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 84 YIVRL 89
Db 220 YIVRL 225

RESULT 12
US-10-467-657-3362
Sequence 3362, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 3362
LENGTH: 243
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3362

Query Match 6.2%; Score 6; DB 6; Length 243;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SLLLA 11
Db 35 SLLLA 40

RESULT 13
US-10-467-657-6
Sequence 6, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 6
LENGTH: 276
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6

Query Match 6.2%; Score 6; DB 6; Length 276;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLLAAL 12
Db 7 LLLAAL 12

Db 26 LLLAAL 31

RESULT 14

US-10-467-657-4158
; Sequence 4158, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4158
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4158

Query Match 6.2%; Score 6; DB 6; Length 276;

Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLLAAL 12

Db 26 LLLAAL 31

RESULT 15

US-10-131-826A-54
; Sequence 54, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-54

Query Match 6.2%; Score 6; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SLLAA 11

Db 5 SLLAA 10

RESULT 16

US-10-821-234-981
; Sequence 981, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 981
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-981

Query Match 6.2%; Score 6; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 IVGFTR 51

Db 214 IVGFTR 219

RESULT 17

US-10-980-388-115
; Sequence 115, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogell, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appli

```

; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 115
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-115

Query Match          6.2%; Score 6; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLLAAL 12
Db 123 LLLAAL 128

RESULT 18
; Sequence 8200, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8200
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8200

Query Match          6.2%; Score 6; DB 6; Length 348;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 47 VGFTTRQ 52
Db 341 VGFTTRQ 346

; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 115
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-115

Query Match          6.2%; Score 6; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLLAAL 12
Db 123 LLLAAL 128

RESULT 19
; Sequence 4740, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4740
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4740

Query Match          6.2%; Score 6; DB 6; Length 356;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLLAAL 12
Db 236 LLLAAL 241

RESULT 20
; Sequence 2136, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2136
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2136

Query Match          6.2%; Score 6; DB 6; Length 358;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SLLLA 11
Db 47 SLLLA 52

RESULT 21
; Sequence 96, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
US-10-980-388-96
```

```
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Huff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 96
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-96

Query Match          6.2%; Score 6; DB 6; Length 358;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLLAAL 12
Db 27 LLLAAL 32

RESULT 22
US-10-793-626-470
; Sequence 470, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 470
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-470

Query Match          6.2%; Score 6; DB 6; Length 365;
Best Local Similarity 100.0%; Pred. No. 29;
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SLLAA 11
Db 54 SLLAA 59

RESULT 23
US-11-108-528-56
; Sequence 56, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Glenn
; APPLICANT: Marvin, Martha
; APPLICANT: Li, Dean Y.
; APPLICANT: Wang, Elizabeth
; APPLICANT: Chen, C. M. Amy
; APPLICANT: Shamah, Steven M.
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-528-56

Query Match          6.2%; Score 6; DB 7; Length 365;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLLAAL 12
Db 19 LLLAAL 24

RESULT 24
US-11-108-528-58
; Sequence 58, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Glenn
; APPLICANT: Marvin, Martha
; APPLICANT: Li, Dean Y.
; APPLICANT: Wang, Elizabeth
; APPLICANT: Chen, C. M. Amy
; APPLICANT: Shamah, Steven M.
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
; FILE REFERENCE: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Mouse
US-11-108-528-58

Query Match          6.2%; Score 6; DB 7; Length 365;
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Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLLAAL 12
Db 19 LLLAAL 24

RESULT 25
US-10-980-388-116
; Sequence 116, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980.388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 116
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-116

Query Match 6.2%; Score 6; DB 6; Length 389;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLLAAL 12
Db 58 LLLAAL 63

Search completed: December 3, 2005, 14:45:49
Job time : 20 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 14:33:51 ; Search time 37 Seconds
(without alignments)
249.643 Million cell updates/sec

Title: US-10-646-770-2

Perfect score: 96

Sequence: 1 MCTKSLLAALMSVLLHL.....PKQTVWKYIVRLLSKKYKNM 96

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	8.3	345	2 F83712	ribonucleoside-dip
2	7	7.3	63	2 E82584	hypothetical prote
3	7	7.3	153	2 A58889	hypothetical 16.2K
4	7	7.3	153	2 D86131	hypothetical prote
5	7	7.3	153	2 G91289	hypothetical prote
6	7	7.3	157	2 C69470	dCMP deaminase hom
7	7	7.3	160	2 B95973	hypothetical expor
8	7	7.3	201	2 T43151	hypothetical prote
9	7	7.3	212	2 F84481	Mutator-like trans
10	7	7.3	238	2 I62385	outer membrane pro
11	7	7.3	240	2 I62394	outer membrane pro
12	7	7.3	241	2 I62387	outer membrane pro
13	7	7.3	241	2 I62391	outer membrane pro
14	7	7.3	243	2 I84531	outer membrane pro
15	7	7.3	243	2 I62388	outer membrane pro
16	7	7.3	335	2 A70128	conserved hypothet
17	7	7.3	346	1 MMECA	outer membrane pro
18	7	7.3	346	2 A30759	outer membrane pro
19	7	7.3	346	2 G85622	outer membrane pro
20	7	7.3	350	2 S07222	outer membrane pro
21	7	7.3	350	2 S51494	arabinogalactan en
22	7	7.3	351	1 MMEBAD	outer membrane pro
23	7	7.3	354	2 E83291	probable secretion
24	7	7.3	356	2 JC6558	outer membrane pro
25	7	7.3	359	2 JC7280	cytokine receptor
26	7	7.3	366	2 G82069	conserved hypothet
27	7	7.3	407	2 F75158	hypothetical prote
28	7	7.3	419	2 G82009	SUN homolog NMA016
29	7	7.3	419	2 B81236	16S RNA methyltran

hypothetical prote
hypothetical prote
dipeptidyl-peptida
chloride channel p
beta-galactoside a
hypothetical prote
two-component sens
H⁺-exporting ATPas
gene 54 protein -
endothelin convert
multidrug resistan
hypothetical prote
probable sensor/re
probable non-ribos
cytochrome P450NMA
spore coat protein
interleukin-2 homo
hypothetical prote
B20L protein - var
hypothetical prote
hypothetical prote
kil protein - phag
kil protein [impor
kil protein [impor
probable kil prote
flagellar biosynth
flagellar biosynth
proline-rich prote
hypothetical 90 pr
LIM1 protein - tru
hypothetical prote
conserved domain p
osteocalcin precur
hypothetical prote
hypothetical prote
conserved hypothet
agcC protein precu
csgC protein precu
probable curli pro
hypothetical prote
probable exported
hypothetical prote
hypothetical HXC-2
hypothetical prote
hypothetical prote
galanin precursor
galanin precursor
calcitonin gene-re
calcitonin gene-re
B48 antigen precu
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hypothetical prote
calcitonin gene-re
hypothetical prote
calcitonin precurs
Ig heavy chain pre
probable secreted
calcitonin precurs
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probable regulator
calcitonin precurs
phospholipase A2 (
Ni,Fe-Hydrogenase
conserved hypothet
hypothetical prote
E6 protein - human
acetyltransferase,
hypothetical prote
hypothetical prote
conserved hypothet

103 6 6.2 160 2 S54747 cysL protein - Bra
104 6 6.2 160 2 T36282 probable tryptophan
105 6 6.2 166 2 B83315 NADH dehydrogenase
106 6 6.2 167 2 A50440 probable carboxydr
107 6 6.2 168 2 E75257 molybdenum cofacto
108 6 6.2 172 2 G82987 secreted protein H
109 6 6.2 172 2 A03857 hypothetical prote
110 6 6.2 174 2 C72737 hypothetical prote
111 6 6.2 180 2 F71284 probable PTS syste
112 6 6.2 181 1 A64477 L-fucose-phospha
113 6 6.2 183 2 D83069 conserved hypotet
114 6 6.2 184 1 S47020 ribosomal protein
115 6 6.2 185 2 F64459 hypothetical prote
116 6 6.2 187 2 C90539 hypothetical prote
117 6 6.2 192 1 KLS88S calcium-binding pr
118 6 6.2 192 2 T09847 phosphoenolpyruvat
119 6 6.2 195 2 H87388 glutathione S-tran
120 6 6.2 202 2 AC3318 sodium-dependent p
121 6 6.2 203 2 AF1199 hypothetical prote
122 6 6.2 203 2 AD1557 hypothetical prote
123 6 6.2 204 2 T39940 GTP cyclohydrolase
124 6 6.2 204 2 T29444 probable two-compo
125 6 6.2 207 2 A10245 probable lipoprote
126 6 6.2 208 2 AC0465 probable membrane
127 6 6.2 210 2 F87492 ATP-dependent Clp
128 6 6.2 210 2 E87512 clpp (AP218420) [i
129 6 6.2 211 2 AE2731 ATP-dependent Clp
130 6 6.2 211 2 AF0011 probable exported
131 6 6.2 212 2 T35272 hypothetical prote
132 6 6.2 212 2 B82125 conserved hypotet
133 6 6.2 213 2 G75303 conserved hypotet
134 6 6.2 218 2 A39375 glutathione transf
135 6 6.2 218 2 F89633 glutamine ABC tran
136 6 6.2 218 2 T40365 conserved hypotet
137 6 6.2 221 2 E64400 conserved hypotet
138 6 6.2 222 2 C75250 hypothetical prote
139 6 6.2 222 2 T36115 probable oxidoredu
140 6 6.2 222 2 C89950 uroporphyrinogen I
141 6 6.2 224 2 T34686 probable integral
142 6 6.2 227 2 S23730 MADS box protein T
143 6 6.2 227 2 T02413 probable RING zinc
144 6 6.2 228 2 C95931 probable amino aci
145 6 6.2 228 2 T32266 hypothetical prote
146 6 6.2 229 2 T05956 germin-like protei
147 6 6.2 229 2 D81867 conserved hypotet
148 6 6.2 229 2 H81073 conserved hypotet
149 6 6.2 230 1 PUSY3 proline-rich prote
150 6 6.2 232 2 T35286 probable methyltra
151 6 6.2 236 2 T36188 hypothetical prote
152 6 6.2 236 2 A13377 25K outer-membrane
153 6 6.2 237 2 T05973 permatin homolog P
154 6 6.2 237 2 B71424 hypothetical prote
155 6 6.2 237 2 A47368 HNF-3/forh head tr
156 6 6.2 239 2 B60537 Ki nuclear autoant
157 6 6.2 240 2 A97826 tRNA/rRNA methyltr
158 6 6.2 240 2 E64897 hypothetical prote
159 6 6.2 240 2 F90885 hypothetical prote
160 6 6.2 240 2 A85733 hypothetical prote
161 6 6.2 241 2 T48006 hypothetical prote
162 6 6.2 243 2 D64300 (R)-2-hydroxygluta
163 6 6.2 243 2 AE3390 hypothetical cytos
164 6 6.2 248 2 AD2687 conserved hypotet
165 6 6.2 248 2 H97468 BH0857 hypothetical
166 6 6.2 248 2 G83238 hypothetical prote
167 6 6.2 249 2 T48603 prohibitin-like pr
168 6 6.2 250 2 T07902 MADS box protein -
169 6 6.2 250 2 T07100 MADS box protein h
170 6 6.2 251 2 D75439 (3R)-hydroxymyrist
171 6 6.2 253 2 T50942 Di-B protein limpo
172 6 6.2 253 2 A10613 probable lipoprote
173 6 6.2 255 2 T28121 hypothetical prote
174 6 6.2 256 2 A29324 proline-rich prote
175 6 6.2 256 2 A11204 molybdate ABC tran

176 6 6.2 259 2 AB3108 outer membrane lip
177 6 6.2 259 2 G98178 probable periplasm
178 6 6.2 261 2 A83281 rpeG protein - syn
179 6 6.2 265 2 S31070 conserved hypotet
180 6 6.2 265 2 H75416 15-hydroxyprostagl
181 6 6.2 266 1 A35802 Ki nuclear autoant
182 6 6.2 267 2 A60537 exopolysaccharide
183 6 6.2 267 2 E87269 hypothetical prote
184 6 6.2 267 2 T06813 hypothetical prote
185 6 6.2 269 2 D64668 hypothetical prote
186 6 6.2 269 2 E72693 hypothetical prote
187 6 6.2 269 2 AH2268 hypothetical prote
188 6 6.2 271 2 G89809 SAM-dependant meth
189 6 6.2 272 2 E96989 membrane protein n
190 6 6.2 273 2 A13630 monofunctional bio
191 6 6.2 273 2 F82846 nosy protein limpo
192 6 6.2 275 2 T44663 unknown protein [i
193 6 6.2 275 2 A86388 hypothetical prote
194 6 6.2 276 2 I39705 endopeptidase Clp
195 6 6.2 277 1 S68421 Outer membrane 30K
196 6 6.2 277 2 JN0751 probable exported
197 6 6.2 277 2 AB0661 phytoene synthetas
198 6 6.2 277 2 G90469 conserved hypotet
199 6 6.2 278 2 E81658 hypothetical prote
200 6 6.2 278 2 A71498 pantote beta-alan
201 6 6.2 283 2 F90066 branched-chain ami
202 6 6.2 285 2 E75539 hypothetical prote
203 6 6.2 288 2 T41112 xap-3-like protein
204 6 6.2 288 2 T40828 conserved hypotet
205 6 6.2 291 2 E82226 hypothetical prote
206 6 6.2 294 2 D83108 hypothetical prote
207 6 6.2 295 2 E75466 ribosomal protein
208 6 6.2 296 2 E71717 hypothetical prote
209 6 6.2 296 2 T20005 lytic enzyme lysA
210 6 6.2 297 2 S38477 urea/short-chain a
211 6 6.2 300 2 F75586 conserved hypotet
212 6 6.2 300 2 H90152 probable binding p
213 6 6.2 302 2 H83478 hypothetical prote
214 6 6.2 303 1 H71246 sugar ABC transpor
215 6 6.2 303 2 AE3520 N-acetylneuraminat
216 6 6.2 305 2 B95154 NADH2 dehydrogenas
217 6 6.2 306 2 T07684 transcription regu
218 6 6.2 306 2 F70389 probable cell divi
219 6 6.2 311 2 C84807 probable cdc2-like
220 6 6.2 311 2 T09586 conserved hypotet
221 6 6.2 313 2 D69336 succinate dehydrog
222 6 6.2 314 1 T50537 NADH dehydrogenase
223 6 6.2 314 2 H84221 dual specificity p
224 6 6.2 314 2 B57126 ferrichrome ABC tr
225 6 6.2 315 1 B69812 highly charged pro
226 6 6.2 315 2 A95275 hypothetical prote
227 6 6.2 315 2 T37273 envelope glycoprot
228 6 6.2 316 2 T23640 conserved hypotet
229 6 6.2 317 2 S68157 conserved hypotet
230 6 6.2 317 2 B83039 sugar ABC transpor
231 6 6.2 317 2 B86183 suhr protein - Rhi
232 6 6.2 318 2 S23155 hypothetical prote
233 6 6.2 319 2 T49458 conserved hypotet
234 6 6.2 321 2 B81668 hypothetical prote
235 6 6.2 321 2 A71510 sugar ABC transpor
236 6 6.2 323 2 C83940 hypothetical prote
237 6 6.2 323 2 A44504 suhr protein - Rhi
238 6 6.2 323 2 T24224 hypothetical prote
239 6 6.2 325 2 H75414 probable ABC trans
240 6 6.2 326 2 T25301 hypothetical prote
241 6 6.2 328 2 T36200 probable DNA polym
242 6 6.2 330 2 JC5717 G protein-coupled
243 6 6.2 330 2 G88115 protein F53C3.1 [i
244 6 6.2 331 2 H95044 sensor histidine k
245 6 6.2 331 2 H95876 probable transcrip
246 6 6.2 331 2 G97914 histidine kinase
247 6 6.2 333 2 B90172 conserved hypotet
248 6 6.2 333 2 G71801 hypothetical prote

249	6	6.2	333	2	H97167	glycosyltransferase	322	6.2	427	2	AH0613	3-phosphoshikimate
250	6	6.2	338	2	T13883	COI intron 1 prote	323	6.2	427	2	A49746	3-phosphoshikimate
251	6	6.2	340	2	S54821	chrB protein - Erw	324	6.2	427	2	E85616	5-enolpyruvylshiki
252	6	6.2	342	2	A24263	myosin heavy chain	325	6.2	427	2	G90752	5-enolpyruvylshiki
253	6	6.2	342	2	T35790	probable transmem	326	6.2	427	2	S13266	3-phosphoshikimate
254	6	6.2	344	2	AG1025	hypothetical prote	327	6.2	427	2	S12096	3-phosphoshikimate
255	6	6.2	344	2	H75452	GGDEF family prote	328	6.2	427	2	E64644	18605 transposase
256	6	6.2	345	2	A13165	ATP-dependent DNA	329	6.2	428	2	AH0169	3-phosphoshikimate
257	6	6.2	346	2	C71390	NADH2 dehydrogenas	330	6.2	428	2	I51087	G protein-coupled
258	6	6.2	348	2	T45071	hypothetical prote	331	6.2	429	2	A86486	protein F28J9.8 [l
259	6	6.2	350	1	VGBB63	glycoprotein gp63	332	6.2	429	2	T01009	hypothetical prote
260	6	6.2	350	2	E72352	N-acetylglucosamin	333	6.2	430	1	XNHUHM	aspartate transami
261	6	6.2	351	2	C82808	lipoprotein precur	334	6.2	430	1	XNR7DM	aspartate transami
262	6	6.2	353	2	A87469	ubiquinol oxidase	335	6.2	432	2	JN0758	3-phosphoshikimate
263	6	6.2	353	2	C64187	outer membrane pro	336	6.2	433	2	A81085	3-phosphoshikimate
264	6	6.2	355	2	C82972	conserved hypothet	337	6.2	433	2	H81858	3-phosphoshikimate
265	6	6.2	356	2	S15156	myosin heavy chain	338	6.2	433	2	S01174	aspartate transami
266	6	6.2	357	2	T25777	hypothetical prote	339	6.2	435	2	E59096	hypothetical prote
267	6	6.2	359	2	G82487	GGDEF family prote	340	6.2	435	2	AF3013	tolB protein [impo
268	6	6.2	360	2	JE0206	deoxyribonuclease	341	6.2	438	2	E83938	allantoicase BH230
269	6	6.2	361	2	F69269	hypothetical prote	342	6.2	439	2	AF1813	hypothetical prote
270	6	6.2	362	2	AF1825	hypothetical prote	343	6.2	440	2	F70792	hypothetical prote
271	6	6.2	364	2	JE0205	deoxyribonuclease	344	6.2	441	2	E81745	conserved hypothet
272	6	6.2	368	2	G86427	probable pectate l	345	6.2	441	2	F71482	hypothetical prote
273	6	6.2	368	2	T39236	Oxidoreductase - f	346	6.2	442	1	XURVRS	3-phosphoshikimate
274	6	6.2	372	2	E72579	probable drug resi	347	6.2	443	2	S44096	enolpyruvylshikima
275	6	6.2	375	2	F75467	probable lipoprote	348	6.2	443	2	A98271	tolB protein precu
276	6	6.2	377	2	B90437	hypothetical prote	349	6.2	444	2	I39294	McLeod syndrome-as
277	6	6.2	379	2	D82481	multidrug resistan	350	6.2	446	2	E81367	probable transmem
278	6	6.2	379	2	S74601	hypothetical prote	351	6.2	447	2	AE0094	probable gluconate
279	6	6.2	379	2	C83996	hypothetical prote	352	6.2	449	2	B69398	hypothetical prote
280	6	6.2	380	2	D82088	chromate resistanc	353	6.2	452	2	E83482	probable MFS trans
281	6	6.2	380	2	S14188	carbonate hydrat	354	6.2	454	2	E75571	chromosomal repli
282	6	6.2	383	2	E81373	hippurate hydrolas	355	6.2	455	2	AH0208	probable transport
283	6	6.2	383	2	I40762	hippurate hydrolas	356	6.2	456	2	T29948	hypothetical prote
284	6	6.2	385	2	C24263	myosin heavy chain	357	6.2	459	2	T04808	hypothetical prote
285	6	6.2	385	2	C64668	hypothetical prote	358	6.2	459	2	D97004	probable cation ef
286	6	6.2	387	2	F82692	conserved hypothet	359	6.2	463	2	B93468	probable sodium/so
287	6	6.2	389	2	TJ37356	leukotriene B4 rec	360	6.2	466	2	B91186	probable permease
288	6	6.2	391	2	P64002	hypothetical prote	361	6.2	466	2	A86033	probable permease
289	6	6.2	392	2	D75432	uroporphyrinogen d	362	6.2	470	2	G85911	hypothetical prote
290	6	6.2	392	2	AF0849	pathogenicity lis	363	6.2	474	1	T05239	acid phosphatase (
291	6	6.2	392	2	S69788	p-gH protein - Sal	364	6.2	474	2	AB2990	polysaccharide bio
292	6	6.2	394	1	S43915	maltose permease -	365	6.2	474	2	G98293	polysaccharide bio
293	6	6.2	395	2	F64534	hypothetical prote	366	6.2	477	2	B75409	multidrug-efflux t
294	6	6.2	398	1	B65126	probable general s	367	6.2	479	2	T23509	hypothetical prote
295	6	6.2	398	2	H64534	hypothetical prote	368	6.2	480	2	A83487	probable MFS trans
296	6	6.2	399	2	D86460	FluM2.17 protein -	369	6.2	481	2	C71338	probable UDP-N-ace
297	6	6.2	400	2	F75275	chromate transport	370	6.2	481	2	AC3281	transporter BMEI02
298	6	6.2	401	2	C83109	probable transport	371	6.2	482	2	B35843	lipopolysaccharide
299	6	6.2	402	2	T37849	hypothetical prote	372	6.2	483	2	S69894	major DNA-binding
300	6	6.2	403	2	R97270	general secretion	373	6.2	484	2	C75609	serine proteinase,
301	6	6.2	404	2	E96745	hypothetical prote	374	6.2	484	2	B75600	amino acid ABC tra
302	6	6.2	406	2	T06805	Kil17-1 protein hom	375	6.2	485	2	C75460	hypothetical prote
303	6	6.2	406	2	JC7798	vacuole membrane p	376	6.2	486	2	JC4028	activating transcr
304	6	6.2	407	2	D83460	cytochrome c-type	377	6.2	488	2	A42491	NADH2 dehydrogenas
305	6	6.2	411	1	ITRT	alpha-1-antitrypsi	378	6.2	488	2	T06259	NADH2 dehydrogenas
306	6	6.2	412	2	D71972	hypothetical prote	379	6.2	488	2	T06260	NADH2 dehydrogenas
307	6	6.2	413	2	A69205	sensory transducti	380	6.2	489	2	S25943	NADH2 dehydrogenas
308	6	6.2	414	2	B96905	hypothetical prote	381	6.2	494	2	B47494	cytochrome P450 2A
309	6	6.2	416	1	ITSH	alpha-1-antitrypsi	382	6.2	494	2	A47494	cytochrome P450 2A
310	6	6.2	416	2	S21097	alpha-1-antitrypsi	383	6.2	494	2	D64944	probable permease
311	6	6.2	417	2	A32128	carboxypeptidase A	384	6.2	494	2	F85794	probable transport
312	6	6.2	417	2	B71034	hypothetical prote	385	6.2	494	2	B90946	probable transport
313	6	6.2	420	2	G95215	xanthine permease	386	6.2	497	2	B71677	histidine kinase s
314	6	6.2	420	2	E98079	nucleobase,cation	387	6.2	497	2	G97738	histidine kinase s
315	6	6.2	420	2	A71327	probable protein-e	388	6.2	498	2	JC8008	betaal-glycosyltran
316	6	6.2	422	2	C70565	hypothetical prote	389	6.2	499	2	T71136	NADH2 dehydrogenas
317	6	6.2	426	2	I39539	3-phosphoshikimate	390	6.2	499	2	S26454	hypothetical prote
318	6	6.2	426	2	D82163	3-phosphoshikimate	391	6.2	500	2	A71306	hypothetical prote
319	6	6.2	427	1	XUEBVS	3-phosphoshikimate	392	6.2	503	2	T06522	trans-cinnamate 4-
320	6	6.2	427	1	XUEBY	3-phosphoshikimate	393	6.2	508	2	F84921	hypothetical prote
321	6	6.2	427	1	XUECVS	3-phosphoshikimate	394	6.2	509	2	S46314	hydroxymethylgluta

395	6	6.2	512	1	W2VZB6	59K HindIII-C prot	468
396	6	6.2	512	2	C42504	C2L protein - vacc	469
397	6	6.2	513	2	T21887	hypothetical prote	470
398	6	6.2	514	2	R69108	phytoene dehydroge	471
399	6	6.2	515	1	A59309	interferon-inducib	472
400	6	6.2	515	2	B84406	TRK potassium upta	473
401	6	6.2	516	1	XUPJVS	3-phosphoshikimate	474
402	6	6.2	516	2	S12744	3-phosphoshikimate	475
403	6	6.2	517	2	A84080	L-arabinose ABC tr	476
404	6	6.2	518	2	S18353	3-phosphoshikimate	477
405	6	6.2	520	1	XUMUVS	3-phosphoshikimate	478
406	6	6.2	520	2	XUTOVS	3-phosphoshikimate	479
407	6	6.2	520	2	H84888	hypothetical prote	480
408	6	6.2	521	2	D96526	hypothetical prote	481
409	6	6.2	522	2	T07118	probable cytochrom	482
410	6	6.2	523	2	D83631	probable sulfate t	483
411	6	6.2	524	2	T02499	hypothetical prote	484
412	6	6.2	527	2	T39741	ars binding protei	485
413	6	6.2	527	2	T18330	hypothetical prote	486
414	6	6.2	528	2	I48253	beta-N-acetylhexos	487
415	6	6.2	529	1	A0HUBA	beta-N-acetylhexos	488
416	6	6.2	531	2	B95180	hypothetical prote	489
417	6	6.2	531	2	F98047	hypothetical prote	490
418	6	6.2	533	2	T34457	hypothetical prote	491
419	6	6.2	533	2	A80146	probable Branched-	492
420	6	6.2	534	2	S38435	hexose transport p	493
421	6	6.2	534	2	S14144	hexose transport p	494
422	6	6.2	543	2	F91067	hypothetical prote	495
423	6	6.2	544	2	H72647	hypothetical prote	496
424	6	6.2	547	2	S19607	alkaline phosphata	497
425	6	6.2	554	2	E95851	probable sensor hi	498
426	6	6.2	555	2	H83043	hypothetical prote	499
427	6	6.2	555	2	T21028	hypothetical prote	500
428	6	6.2	556	2	T49501	hypothetical prote	501
429	6	6.2	557	1	H64240	hypothetical prote	502
430	6	6.2	557	2	A61256	myosin heavy chain	503
431	6	6.2	563	1	HMTVCV	hemagglutinin prec	504
432	6	6.2	563	1	HMTVSV	hemagglutinin prec	505
433	6	6.2	566	2	A84485	hypothetical prote	506
434	6	6.2	572	2	S73901	ABC transporter YJ	507
435	6	6.2	573	2	C95856	probable dihydroxy	508
436	6	6.2	573	2	H86513	protein F2H15.10 [509
437	6	6.2	583	2	I39428	alcam - human	510
438	6	6.2	585	2	A46507	Ig alpha chain - c	511
439	6	6.2	586	2	T19075	hypothetical prote	512
440	6	6.2	586	2	T47620	histon acetyltrans	513
441	6	6.2	586	2	AH2133	ATP-binding protei	514
442	6	6.2	587	2	T06518	chaperonin 60 alph	515
443	6	6.2	588	2	JH0506	adhesion molecule	516
444	6	6.2	588	2	A45254	surface glycoprote	517
445	6	6.2	595	2	A10042	thiol/disulfide in	518
446	6	6.2	602	2	A42986	phosphogluconate d	519
447	6	6.2	603	2	A10741	phosphogluconate d	520
448	6	6.2	603	2	A98949	6-phosphogluconate	521
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450	6	6.2	606	2	T31557	hypothetical prote	523
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452	6	6.2	613	2	T00077	gag-like protein -	525
453	6	6.2	615	2	AQ0552	protein-export mem	526
454	6	6.2	620	2	T27008	hypothetical prote	527
455	6	6.2	626	2	E82314	methyl-accepting c	528
456	6	6.2	644	2	A36325	epidermal growth f	529
457	6	6.2	648	2	S18666	gene H19 protein -	530
458	6	6.2	653	2	D82352	iron(III) ABC tran	531
459	6	6.2	672	2	A56765	sodium-glucose cot	532
460	6	6.2	672	2	A42251	nucleoside transpo	533
461	6	6.2	672	2	A65024	Hydrogenase-4 comp	534
462	6	6.2	672	2	D85891	hydrogenase-4 memb	535
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464	6	6.2	673	2	S06048	poly(glycerol)-phos	537
465	6	6.2	683	2	H72227	translation elonga	538
466	6	6.2	689	2	A83036	conserved hypothet	539
467	6	6.2	689	2	E87376	penicillin amidase	540
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						hypothetical prote	552
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						hypothetical prote	554
						potassium channel	555
						C14orf4 protein -	556
						competence protein	557
						protease TMP - t	558
						probable sensor ki	559
						potassium channel	560
						integrin beta chai	561
						probable efflux pr	562
						probable ATP-depen	563
						phosphoenolpyruvat	564
						ORF MSV089 probabl	565
						invasin - Versinia	566
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						probable nucleopor	568
						hypothetical prote	569
						conserved hypothet	570
						phosphoenolpyruvat	571
						DNA-directed RNA p	572
						tpoC protein homol	573
						probable capsid-as	574
						cell division prot	575
						protein-tyrosine k	576
						H+-exporting ATPase	577
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						probable pyruvate	581
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						S/T protein kinase	585
						probable membrane	586
						RNA-directed DNA p	587
						mutL protein homol	588
						pyruvate dehydroge	589
						TonB-dependent rec	590
						phosphoenolpyruvat	591
						thrombospondin 4 p	592
						integrin beta-4 pr	593
						hypothetical prote	594
						dna exoribonucleas	595
						hypothetical prote	596
						Ca2+-transporting	597
						Ca2+-transporting	598
						alpha-mannosidase	599
						hypothetical prote	600
						ATP-dependent DNA	601
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						rnd multidrug effl	603
						RND multidrug effl	604
						ACR/ABC/ABC fam	605
						hypothetical prote	606
						adenylate cyclase	607
						phenylalanine race	608
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						transmembrane prot	612

541 6 6.2 1132 2 S60433 probable membrane
542 6 6.2 1133 1 GNVUSR M polyprotein prec
543 6 6.2 1133 1 A43964 M polyprotein prec
544 6 6.2 1133 2 S12597 M polyprotein prec
545 6 6.2 1134 1 A43960 M polyprotein prec
546 6 6.2 1134 1 GNVU22 M polyprotein prec
547 6 6.2 1158 2 T43519 condensin complex
548 6 6.2 1174 1 HUBYDH helicase (EC 3.6.1
549 6 6.2 1174 2 S28976 DNA-directed RNA p
550 6 6.2 1182 2 I48378 hairless protein -
551 6 6.2 1193 2 E88445 protein C26E6.4 [i
552 6 6.2 1196 2 T13057 KIAA0729 protein -
553 6 6.2 1202 2 T17197 adenylate cyclase
554 6 6.2 1216 2 H84629 hypothetical prote
555 6 6.2 1236 2 T19492 hypothetical prote
556 6 6.2 1247 2 A33812 interphotoreceptor
557 6 6.2 1286 2 A42150 P-glycoprotein pgp
558 6 6.2 1292 2 P64237 DNA-directed RNA p
559 6 6.2 1445 2 T50508 hypothetical prote
560 6 6.2 1473 2 A90116 DNA-directed RNA p
561 6 6.2 1520 2 A81731 polymorphic membra
562 6 6.2 1747 2 T43162 vitellogenin - gyp
563 6 6.2 1828 2 B59254 myosin heavy chain
564 6 6.2 1853 1 A46761 myosin heavy chain
565 6 6.2 1855 2 A59254 myosin heavy chain
566 6 6.2 1870 2 A36429 integrin beta-4 ch
567 6 6.2 1945 1 A24922 myosin heavy chain
568 6 6.2 1940 1 S04090 myosin heavy chain
569 6 6.2 1956 2 T16416 hypothetical prote
570 6 6.2 2124 2 H83357 probable non-ribos
571 6 6.2 2225 2 T26063 hypothetical prote
572 6 6.2 2616 2 A57096 nudel protein prec
573 6 6.2 3104 2 S20473 fatty-acid synthas
574 6 6.2 3430 1 GNVWV genome polyprotein
575 6 6.2 3433 1 GNVKV genome polyprotein
576 6 6.2 3434 1 GNVWV genome polyprotein
577 6 6.2 3705 2 A00123 probable autocrans
578 6 6.2 4085 2 S28600 hypothetical prote
579 6 6.2 4096 2 A57099 DNA-activated prot
580 6 6.2 4128 2 JC6306 protein kinase (EC
581 6 6.2 5170 2 T15348 hypothetical prote

ALIGNMENTS

RESULT 1
F83712
ribonucleoside-diphosphate reductase beta subunit nrdb - Bacillus halodurans
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C/Accession: F83712
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: F83712
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-345 <STO>
A/Cross-references: UNIPROT:Q9KPH7; UNIPARC:UPI0000133978; GB:AP001508; GB:BA0000004; NID
A/Experimental source: strain C-125
C/Genetics:
A/Gene: nrdb
C/Superfamily: ribonucleoside diphosphate reductase beta chain

Query Match 8.3%; Score 8; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LAALMSVL 16
|||||||
Db 107 LAALMSVL 114

RESULT 2

B82584
hypothetical protein XF2231 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: B82584
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: B82584
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-63 <SIM>
A/Cross-references: UNIPROT:Q9PBB3; UNIPARC:UPI000000C2998; GB:AE004035; GB:AE003849; NID
A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
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submitted to GenBank, June 2000
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Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A/Reference number: A59328
A/Contents: annotation
C/Genetics:
A/Gene: XF2231

Query Match 7.3%; Score 7; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SLLLAAL 12
|||||||
Db 36 SLLLAAL 42

RESULT 3

A55889
hypothetical 16.2K protein (iada-mcrD intergenic region) - Escherichia coli (strain K-12)
N/Alternate names: hypothetical protein f153 (iada 5' region)
C/Species: Escherichia coli
C/Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C/Accession: A55889; S56554; C65247
R/Gary, J.D.; Clarke, S
J. Biol. Chem. 270, 4076-4087, 1995
A/Title: Purification and characterization of an isopartyl dipeptidase from Escherichia
A/Reference number: A55889; MUID:95181377; PMID:7876157
A/Accession: A55889
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-153 <GAP>
A/Cross-references: UNIPROT:P39378; UNIPARC:UPI000013B5B0; GB:U15029; NID:9640029; PIDN:
R/Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A/Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8
A/Reference number: S56314; MUID:95334362; PMID:7610040
A/Accession: S56354
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-153 <BUR>
A/Cross-references: UNIPARC:UPI000013B5B0; EMBL:U14003; NID:gl263172; PIDN:AAA97225.1; P
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: C65247
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-153 <BLAT>
A:Cross-references: UNIPARC:UPI000013B5B0; GB:AE000503; GB:U00096; NID:gl790777; PIDN:AA
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: yjiG
C:Superfamily: spore maturation protein, SpmB type

Query Match 7.3%; Score 7; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLAALMS 14
| | | | |
72 LLAALMS 78

Db

RESULT 4

D86131
hypothetical protein yjiG [imported] - *Escherichia coli* (strain O157:H7, substrain EDL933)
C:Species: *Escherichia coli*
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D86131
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dinalanta, E.; Potamouis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D86131
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-153 <STO>
A:Cross-references: UNIPROT:P39378; UNIPARC:UPI000013B5B0; GB:AE0005174; NID:gl2519340; E
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yjiG
C:Superfamily: spore maturation protein, SpmB type

Query Match 7.3%; Score 7; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLAALMS 14
| | | | |
72 LLAALMS 78

Db

RESULT 5

G91289
hypothetical protein EGc5287 [imported] - *Escherichia coli* (strain O157:H7, substrain R1
C:Species: *Escherichia coli*
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: G91289
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: G91289
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-153 <HAY>
A:Cross-references: UNIPROT:P39378; UNIPARC:UPI000013B5B0; GB:BA000007; PIDN:BAE38710.1;
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: EGc5287
C:Superfamily: spore maturation protein, SpmB type

Query Match 7.3%; Score 7; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SLLAAL 12

Query Match 7.3%; Score 7; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLAALMS 14
| | | | |
72 LLAALMS 78

Db

RESULT 6

C69470
dCMP deaminase homolog - *Archaeoglobus fulgidus*
C:Species: *Archaeoglobus fulgidus*
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: C69470
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.;
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: C69470
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-157 <KLE>
A:Cross-references: UNIPROT:O28510; UNIPARC:UPI0000056BDA; GB:AE000981; GB:AE000782; NID
C:Superfamily: *Archaeoglobus* probable dCMP deaminase

Query Match 7.3%; Score 7; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 LSKKVK 95
| | | | |
151 LSKKVK 157

Db

RESULT 7

B95973
hypothetical exported protein [imported] - *Sinorhizobium meliloti* (strain 1021) magaplae
C:Species: *Sinorhizobium meliloti*
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: B95973
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-Kb pSymb megaplaemid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: B95973
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-160 <KUR>
A:Cross-references: UNIPROT:Q92UP5; UNIPARC:UPI00000CB743; GB:AL591985; PIDN:CAC49450.1;
A:Experimental source: strain 1021, megaplaemid pSymb
R:Galibert, P.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SWb20927
A:Genome: plasmid

Query Match 7.3%; Score 7; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SLLAAL 12

```
Db      10 SLLLAAL 16
|||||
RESULT 8
T43151
hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)
C:Species: Schizosaccharomyces pombe
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43151
R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:98162722; PMID:9501991
A:Accession: T43151
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-201 <YOS>
A:Cross-references: UNIPROT:P78893; UNIPARC:UPI000006A723; EMBL:D89244; NID:gl749695; PID:
A:Experimental source: strain PR745

Query Match      7.3%; Score 7; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      14 SVLLLHL 20
        |||||
Db      189 SVLLLHL 195

RESULT 9
F84481
Mutator-like transposase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: F84481
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84481
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-212 <STO>
A:Cross-references: UNIPROT:Q9ZVW8; UNIPARC:UPI00000A832B; GB:AE002093; NID:g3779027; PID:
A:Gene: At2g07030
A:Map position: 2

Query Match      7.3%; Score 7; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      85 IVRLLSK 91
        |||||
Db      76 IVRLLSK 82

RESULT 10
I62385
outer membrane protein ompA - Escherichia vulneris (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia vulneris
C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: I62385
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: I40701; MUID:92065252; PMID:1955870
A:Accession: I62385
A:Status: preliminary; translated from GB/EMBL/DBDJ

Db      10 SLLLAAL 16
|||||
RESULT 8
T43151
hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)
C:Species: Schizosaccharomyces pombe
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43151
R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:98162722; PMID:9501991
A:Accession: T43151
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-201 <YOS>
A:Cross-references: UNIPROT:P78893; UNIPARC:UPI000006A723; EMBL:D89244; NID:gl749695; PID:
A:Experimental source: strain PR745

Query Match      7.3%; Score 7; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      14 SVLLLHL 20
        |||||
Db      189 SVLLLHL 195

RESULT 9
F84481
Mutator-like transposase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: F84481
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84481
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-212 <STO>
A:Cross-references: UNIPROT:Q9ZVW8; UNIPARC:UPI00000A832B; GB:AE002093; NID:g3779027; PID:
A:Gene: At2g07030
A:Map position: 2

Query Match      7.3%; Score 7; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      85 IVRLLSK 91
        |||||
Db      76 IVRLLSK 82

RESULT 10
I62385
outer membrane protein ompA - Escherichia vulneris (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia vulneris
C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: I62385
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: I40701; MUID:92065252; PMID:1955870
A:Accession: I62385
A:Status: preliminary; translated from GB/EMBL/DBDJ
```

```
A:Molecule type: DNA
A:Residues: 1-238 <RES>
A:Cross-references: UNIPROT:Q99114; UNIPARC:UPI00000B0580; GB:M63348; NID:gl46984; PID:
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:98-109/Region: alanine/proline-rich

Query Match      7.3%; Score 7; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      34 LGYTDRI 40
        |||||
Db      159 LGYTDRI 165

RESULT 11
I62394
outer membrane protein ompA - Escherichia blattae (ATCC 33430) (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia blattae
A:Variety: ATCC 33430
C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: I62394
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: I40701; MUID:92065252; PMID:1955870
A:Accession: I62394
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-240 <RES>
A:Cross-references: UNIPROT:Q99124; UNIPARC:UPI000016EC3C; GB:M63345; NID:gl47002; PID:
A:Experimental source: ATCC 33430
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:100-111/Region: alanine/proline-rich

Query Match      7.3%; Score 7; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      34 LGYTDRI 40
        |||||
Db      161 LGYTDRI 167

RESULT 12
I62387
outer membrane protein A - Escherichia blattae (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia blattae
C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: I62387
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: I40701; MUID:92065252; PMID:1955870
A:Accession: I62387
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-241 <RES>
A:Cross-references: UNIPROT:Q99124; UNIPARC:UPI0000130CF2; GB:M63343; NID:gl46988; PID:
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:101-112/Region: alanine/proline-rich
```

```
Query Match          7.3%; Score 7; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 34 LGYTDRI 40
Db 162 LGYTDRI 168

RESULT 13
outer membrane protein A - Escherichia biattae (ATCC 33429) (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia biattae
A;Variety: ATCC 33429
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I62391
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I62391
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-241 <RES>
A;Cross-references: UNIPROT:Q99124; UNIPARC:UPI000016EC3B; GB:M63344; NID:gl46996; PIDN:
A;Experimental source: ATCC 33429
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;101-112/Region: alanine/proline-rich

Query Match          7.3%; Score 7; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 34 LGYTDRI 40
Db 162 LGYTDRI 168

RESULT 14
outer membrane protein A - Escherichia fergusonii (ATCC 35469) (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia fergusonii
A;Variety: ATCC 35469
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I84531
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I84531
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-243 <RES>
A;Cross-references: UNIPROT:P24747; UNIPARC:UPI0000130CF3; GB:M63351; NID:gl46982; PIDN:
A;Experimental source: ATCC 35469
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;103-114/Region: alanine/proline-rich

Query Match          7.3%; Score 7; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 34 LGYTDRI 40
Db 164 LGYTDRI 170

RESULT 15
outer membrane protein A - Escherichia fergusonii (ATCC 35472) (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia fergusonii
A;Variety: ATCC 35472
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I62388; I62392
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I62388
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-243 <RES>
A;Cross-references: UNIPROT:P24747; UNIPARC:UPI0000130CF3; GB:M63352; NID:gl46990; PIDN:
A;Experimental source: ATCC 35471
A;Accession: I62392
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-243 <RES>
A;Cross-references: UNIPARC:UPI0000130CF3; GB:M63353; NID:gl46998; PIDN:AAA24240.1; PID:
A;Experimental source: ATCC 35472
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;103-114/Region: alanine/proline-rich

Query Match          7.3%; Score 7; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 34 LGYTDRI 40
Db 164 LGYTDRI 170

RESULT 16
conserved hypothetical protein BB0225 - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Oct-2004
C;Accession: A70128
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kervage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vglt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: A70128
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-335 <KLE>
A;Cross-references: UNIPROT:O51243; UNIPARC:UPI00000573CB; GB:AE001133; GB:AE000783; NID
A;Experimental source: strain B31
C;Superfamily: tRNA-dihydrouridine synthase

Query Match          7.3%; Score 7; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 87 RLSSKV 93
Db 25 RLSSKV 31

RESULT 17
MMECA
```


outer membrane protein A precursor - Escherichia coli (strain K-12)
N;Alternate names: outer membrane protein II*
C;Species: Escherichia coli
C;Date: 30-Sep-1980 #sequence_revision 30-Sep-1980 #text_change 09-Jul-2004
C;Accession: A93707; A92862; A93855; S50909; D64836; A03434
R;Beck, E.; Bremer, E.
Nucleic Acids Res. 8, 3011-3024, 1980
A;Title: Nucleotide sequence of the gene ompA coding the outer membrane protein II of Escherichia coli
A;Reference number: A93707; MUID:81053729; PMID:6253901
A;Accession: A93707
A;Molecule type: DNA
A;Residues: 1-346 <BEC>
A;Cross-references: UNIPROT:P02934; UNIPARC:UPI0000130CF0; GB:J01654; NID:G42
A;Experimental source: strain K12
R;Movva, N.R.; Nakamura, K.; Inouye, M.
J. Mol. Biol. 143, 317-328, 1980
A;Title: Gene structure of the OmpA protein, a major surface protein of Escherichia coli
A;Reference number: A92862; MUID:81170587; PMID:6260961
A;Accession: A92862
A;Molecule type: DNA
A;Residues: 1-346 <MOV>
A;Cross-references: UNIPARC:UPI0000130CF0; GB:J01654; GB:V00307; GB:V00358; NID:G146979;
A;Experimental source: K12, strain K802
R;Chen, R.; Schmidmayr, W.; Kramer, C.; Chen-Schmeisser, U.; Henning, U.
Proc. Natl. Acad. Sci. U.S.A. 77, 4592-4596, 1980
A;Title: Primary structure of major outer membrane protein II* (ompA protein) of Escherichia coli
A;Reference number: A93855; MUID:81054820; PMID:7001461
A;Accession: A93855
A;Molecule type: protein
A;Residues: 22-346 <CHE>
A;Cross-references: UNIPARC:UPI000017472B
A;Experimental source: K12, strain P400
R;Kuhn, A.; Kiefer, D.; Koehne, C.; Zhu, H.Y.; Tschantz, W.R.; Dalbey, R.E.
Eur. J. Biochem. 226, 891-897, 1994
A;Title: Evidence for a loop-like insertion mechanism of pro-Omp A into the inner membrane
A;Reference number: S50909; MUID:95112855; PMID:7813480
A;Accession: S50909
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-46 <KUH>
A;Cross-references: UNIPARC:UPI000017472C
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: D64836
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-346 <BLAT>
A;Cross-references: UNIPARC:UPI0000130CF0; GB:AE000198; GB:U000096; NID:G1787189; PIDN:AA
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: ompA; tolG; tut; con
A;Map position: 22 min
C;Function:
A;Description: required for the action of colicins K and L and for the stabilization of diffusion channels that allow penetration of various solutes
C;Superfamily: outer membrane protein A
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-346/Product: outer membrane protein A #status predicted <MAT>
F;22-196/Domain: intramembrane #status predicted <INT>
F;196-208/Region: alanine/proline-rich
F;209-346/Domain: periplasmic #status predicted <PER>
F;257-301/Domain: ompA-like domain #status predicted <OMP>

Query Match 7.3%; Score 7; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 LGYTDR 40
|||||

Db 258 LGYTDR 264

RESULT 18

A90759

outer membrane protein 3a [imported] - Escherichia coli (strain O157:H7, substrain ECs1041)

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: A90759

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;

Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: A90759

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-346 <HAY>

A;Cross-references: UNIPROT:P02934; UNIPARC:UPI0000130CF0; GB:BA000007; PIDN:BA034464.1;

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs1041

C;Superfamily: outer membrane protein A

Query Match 7.3%; Score 7; DB 2; Length 346;

Best Local Similarity 100.0%; Pred. No. 44;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 LGYTDR 40

|||||

Db 258 LGYTDR 264

RESULT 19

G85622

outer membrane protein 3a [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: G85622

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew,

Iller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: G85622

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-346 <STO>

A;Cross-references: UNIPROT:P02934; UNIPARC:UPI0000130CF0; GB:AE005174; NID:G12514142; P1

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: ompA

C;Superfamily: outer membrane protein A

Query Match 7.3%; Score 7; DB 2; Length 346;

Best Local Similarity 100.0%; Pred. No. 44;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 LGYTDR 40

|||||

Db 258 LGYTDR 264

RESULT 20

S07222

outer membrane protein ompA precursor - Enterobacter aerogenes

C;Species: Enterobacter aerogenes

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004

C;Accession: S07222

R;Braun, G.; Cole, S.T.

Eur. J. Biochem. 137, 495-500, 1983

A;Title: Molecular characterization of the gene coding for major outer membrane protein C

A;Reference number: S07222; MUID:84108348; PMID:6363059

```
A;Accession: S07222
A;Molecule type: DNA
A;Residues: 1-350 <BRA>
A;Cross-references: UNIPROT:P09146; UNIPARC:UPI0000130CF1; EMBL:X00254; NID:G40837; PIDN:
A;Note: the authors translated the codon CAG for residue 197 as Asn
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-350/Product: outer membrane protein ompA #status predicted <MAT>
F;201-212/Region: alanine/proline-rich
F;213-350/Domain: periplasmic #status predicted <PER>

Query Match 7.3%; Score 7; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 LGYTDR1 40
Db 262 LGYTDR1 268

RESULT 21
S51494
arabinogalactan endo-1,4-beta-galactosidase - Aspergillus aculeatus
C;Species: Aspergillus aculeatus
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51494
R;Christgau, S.; Sandal, T.; Kofod, L.V.; Dalboge, H.
Curr. Genet. 27, 135-141, 1995
A;Title: Expression cloning, purification and characterization of a beta-1,4-galactanase
A;Reference number: S51494; MUID:95308535; PMID:7788716
A;Accession: S51494
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-350 <CHR>
A;Cross-references: UNIPROT:P48842; UNIPARC:UPI000012BOCE; EMBL:L34599; NID:G509836; PIDN:
C;Genetics:
A;Gene: gall

Query Match 7.3%; Score 7; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SLLLAAL 12
Db 4 SLLLAAL 10

RESULT 22
MMEBAD
outer membrane protein A precursor - Shigella dysenteriae
C;Species: Shigella dysenteriae
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A03435
R;Braun, G.; Cole, S.T.
Nucleic Acids Res. 10, 2367-2378, 1982
A;Title: The nucleotide sequence coding for major outer membrane protein OmpA of Shigella
A;Reference number: A03435; MUID:82221414; PMID:6283478
A;Accession: A03435
A;Molecule type: DNA
A;Residues: 1-351 <BRA>
A;Cross-references: UNIPROT:P02935; UNIPARC:UPI0000130CFA; GB:V01344; NID:G46943; PIDN:
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-351/Product: outer membrane protein A #status predicted <MAT>
F;22-201/Domain: intramembrane #status predicted <INT>
F;201-213/Region: alanine/proline-rich
F;214-351/Domain: periplasmic #status predicted <PER>
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Query Match 7.3%; Score 7; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 LGYTDR1 40
Db 263 LGYTDR1 269

RESULT 23
E83291
probable secretion protein PA2836 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E83291
R;Stover, C.K.; Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brj-
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83291
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-354 <STO>
A;Cross-references: UNIPROT:Q91007; UNIPARC:UPI00000C5834; GB:AE004710; GB:AE004091; NID:
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2836
C;Superfamily: multidrug resistance protein A; lipoyl/biotin-binding homology

Query Match 7.3%; Score 7; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SLLLAAL 12
Db 10 SLLLAAL 16

RESULT 24
JC6558
outer membrane protein A precursor - Klebsiella pneumoniae
C;Species: Klebsiella pneumoniae
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
C;Accession: JC6558
R;Nguyen, T.N.; Samuelson, P.; Sterky, F.; Merle-Poitte, C.; Robert, A.; Baussant, T.; Ha-
Gene 210, 93-101, 1998
A;Title: Chromosomal sequencing using a PCR-based biotin-capture method allowed isolation
A;Reference number: JC6558; MUID:98192544; PMID:9524233
A;Accession: JC6558
A;Molecule type: DNA
A;Residues: 1-356 <NGU>
A;Cross-references: UNIPARC:UPI00001780DF
A;Experimental source: IP 1145
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-356/Product: outer membrane protein A #status predicted <MAT>

Query Match 7.3%; Score 7; DB 2; Length 356;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 LGYTDR1 40
Db 268 LGYTDR1 274

RESULT 25
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JC7280
cytokine receptor-like molecule-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: JC7280
R:Hiroshima, T.; Iwama, A.; Morita, Y.; Nakamura, Y.; Shibuya, A.; Nakauchi, H.
Biochem. Biophys. Res. Commun. 272, 224-229, 2000
A:Title: Molecular cloning and characterization of CRLM-2, a novel type I cytokine receptor
A:Reference number: JC7280
A:Contents: Embryo
A:Accession: JC7280
A:Molecule type: mRNA
A:Residues: 1-359 <HIR>
A:Cross-references: UNIPARC:UPI000017C648; DDBJ:AB039945
C:Genetics:
A:Gene: crlm-2
C:Keywords: cytokine; embryo; receptor; signal transduction; transmembrane protein

Query Match 7.3%; Score 7; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SLLLAAL 12
DB 247 SLLLAAL 253

Search completed: December 3, 2005, 14:44:49
Job time : 56 secs

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